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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Sutcliffe, J. Gregor
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- (ii) TITLE OF INVENTION: Hypothalamus-Specific Polypeptides
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Olson & Hierl, Ltd.
 - (B) STREET: 20 North Wacker Drive, 36th Floor
 - (C) CITY: Chicago
 - (D) STATE: IL
 - (E) COUNTRY: USA
 - (F) ZIP: 60606
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 01-AUG-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/023,220
 - (B) FILING DATE: 02-AUG-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Arne M. Olson
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 - (C) REFERENCE/DOCKET NUMBER: 548.1P
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asn Leu Pro Ser Thr Lys Val Pro Trp Ala Ala Val Thr Leu Leu
 1 5 10 15
 Leu Leu Leu Leu Leu Pro Pro Ala Leu Leu Ser Leu Gly Val Asp Ala
 20 25 30
 Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr Cys Ser Cys Arg Leu
 35 40 45
 Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala Ala Gly Ile Leu Thr
 50 55 60 *Thr*
 Leu Gly Lys Arg Arg Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln
 65 70 75 80
 Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met
 85 90 95
 Gly Arg Arg Ala Gly Ala Glu Leu Glu Pro Tyr Pro Cys Pro Gly Arg
 100 105 110
 Arg Cys Pro Thr Ala Thr Ala Thr Ala Leu Ala Pro Arg Gly Gly Ser
 115 120 125
 Arg Val
 130

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asn Phe Pro Ser Thr Lys Val Pro Trp Ala Ala Val Thr Leu Leu
 1 5 10 15
 Leu Leu Leu Leu Leu Pro Pro Ala Leu Leu Ser Leu Gly Val Asp Ala
 20 25 30
 Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr Cys Ser Cys Arg Leu
 35 40 45
 Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala Ala Gly Ile Leu Thr
 50 55 60

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Leu Gly Lys Arg Arg Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln
 65 70 75 80
 Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met
 85 90 95
 Gly Arg Arg Ala Gly Ala Glu Leu Glu Pro His Pro Cys Ser Gly Arg
 100 105 110
 Gly Cys Pro Thr Val Thr Thr Thr Ala Leu Ala Pro Arg Gly Gly Ser
 115 120 125
 Gly Val
 130

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 569 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TAAGACGACG GCCTCAGACT CCTGGGTAT TTGGACCACT GCACCGAAGA TACCATCTCT	60
CCGGATTACC TCTCCCTGAG CTCCAGACAC CATGAACCTT CCTTCTACAA AGGTTCCCTG	120
GGCCGCCGTG ACGCTGCTGC TGCTGCTACT GCTGCCGCCG GCGCTGCTGT CGCTTGGGGT	180
GGACGCGCAG CCTCTGCCCC ACTGCTGTCT CCAGAAGACG TGTTCCTGCC GGCTCTACGA	240
ACTGTTGCAC GGAGCTGGCA ACCACGCCGC GGGCATCCTC ACTCTGGGAA AGCGGCGACC	300
TGGACCCCCA GGCCTCCAAG GACGGCTGCA GCGCCTCCTT CAGGCCAACG GTAACCACGC	360
AGCTGGCATC CTGACCATGG GCCGCCCGGC AGGCGCAGAG CTAGAGCCAT ATCCCTGCCC	420
TGGTCGCCGC TGTCCGACTG CAACCGCCAC CGCTTTAGCG CCCCAGGGCG GATCCAGAGT	480
CTGAACCCGT CTTCTATCCC TGTCTAGTC CTAACCTTCC CCTCTCCTCG CCAGTCCCTA	540
GGCAATAAAG ACGTTTCTCT GTTGCTGTG	569

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 582 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TAAGACGACG GCCTCAGACT TCTTGGGTAT TTGGACCACT GCACTGAAGA GATCATCTCT	60
CCAGATTACT TTCCCCTGAG CTCCAGGCAC CATGAACTTT CCTTCTACAA AGGTTCCCTG	120
GGCCGCCGTG ACGCTGCTGC TGCTGCTACT GCTGCCACCG GCGCTGCTGT CGCTTGGGGT	180
GGACGCACAG CCTCTGCCCC ACTGCTGTCTG CCAGAAGACG TGTTCTGCTG GTCTCTACGA	240
ACTGTTGCAC GGAGCTGGCA ACCACGCTGC GGGTATCCTG ACTCTGGGAA AGCGGCGGCC	300
TGGACCTCCA GGCTCCAGG GACGGCTGCA GCGCCTCCTT CAGGCCAACG GTAACCACGC	360
AGCTGGCATC CTGACCATGG GCCGCCGCGC AGGCGCAGAG CTAGAGCCAC ATCCCTGCTC	420
TGGTCGCGGC TGTCCGACCG TAACTATCAC CGCTTTAGCA CCCCAGGGAG GGTCCGGAGT	480
TTGAACCCAT CTTCTATCCT TGTCCTGATC CAAACTTCCC CCTCTGCTCG CCGCTGTCAG	540
TCTCTTGGA AATGGCAATA AAGACGTTT TCTGTTGGTG TG	582

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTAGGAGAC ATTGCGGCGG CGGTGGCGGC GTTGGCAGCA GCTGCAGACA TGCTGCTGCT	60
CAAGAAACAG ACGGAGGACA TCAGCAGTGT CTATGAGATC CGGGAGAAGC TGGGCTCGGG	120
TGCCTTCTCT GAGGTGATGC TGGCCCAGGA AAGGGGCTCT GCTCATCTTG TGGCCCTCAA	180
GTGCATTCCC AAGAAAGCAC TTCGGGGCAA GGAGGCCCTG GTGGAGAATG AGATCGCAGT	240
ACTCCGCAGG ATTAGCCACC CCAACATTGT GGCTCTGGAG GACGTCCACG AGAGCCCTTC	300
CCATCTCTAC TTGGCCATGG AGCTGGTAAC AGGTGGTGAA CTGTTTGACC GAATCATGGA	360
GCGGGGCTCC TACACAGAGA AGGATGCGAG CCACCTTGTA GGGCAGGTCC TTGGTGCTGT	420

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CTCCTACCTT CATAGCCTGG GCATCGTGCA CCGGGACCTC AAGCCTGAAA ACCTCCTCTA	480
TGCCACACCT TTTGAGGACT CCAAGATCAT GGTCTCTGAC TTTGGCCTGT CCAAAATTCA	540
AGCTGGCAAC ATGCTAGGCA CAGCCTGTGG GACCCCAGGA TATGTGGCCC CAGAGCTCCT	600
GGAGCAGAAA CCCTACGGGA AGGCCGTAGA TGTGTGGGCC CTGGGTGTCA TCTCCTACAT	660
CCTGCTGTGT GGGTACCCCC CCTTCTATGA TGAGAGCGAT CCTGAACTCT TCAGCCAGAT	720
TCTGAGGGCC AGCTACGAGT TTGACTCTCC CTTTGGGAT GACATCTCAG AATCAGCCAA	780
AGACTTCATT CGGCACCTTC TGAACGTGA TCCCCAGAAG AGGTTACCT GCCAACAGGC	840
CTTACAGCAT CTCTGGATCT CTGGGGATGC AGCCTTGGAC AGGGACATCC TAGGTTCTGT	900
CAGTGAGCAG ATCCAGAAGA ATTTTGCCAG GACCCACTGG AAGCGTGCAT TCAATGCCAC	960
ATCATTCCTA CGTCACATCC GTAAGCTGGG ACAGAGCCCA GAGGGTGAGG AGGCCTCCAG	1020
GCAGGGTATG ACCCGTCACA GCCACCCAGG CCTTGGGACT AGCCAGTCTC CCAAGTGGTG	1080
ACAACCAGGT GGATGCCAAG GAAGGCCAAG TGGACTGACT CCTAGCTTTT CTTTCTCCA	1140
GCCCTTTTGA TCTCCTTCCC TGATCCTTGT CCCCCGACT GGCCTCTGTT GGAAAGTCCA	1200
AGACCGTGGG TGTGATGCAT GGCACTGGGG TATGGGGCTT CCCAAGTATG TCCCCAGCCT	1260
CTGTCTTTG TTGCTGCCAC CCTCTATGGA AACTGAGGAG GTATTCAAAA ATGGATTTGG	1320
GGGCCATCCT TCCTGCACCT TGCACGCACA TATGCATTGC GTGGCTGTTT TGTGCTTTGC	1380
TGACTGTGGG TGGTCCTGCT TGTGTTGTAG CCCTTTAGTT CCTCCTCTTT CCAACCAATA	1440
AAGACAAACA GAACAATG	1458

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu	Gly	Val	Asp	Ala	Gln	Pro	Leu	Pro	Asp	Cys	Cys	Arg	Gln	Lys	Thr
1				5					10					15	
Cys	Ser	Cys	Arg	Leu	Tyr	Glu	Leu	Leu	His	Gly	Ala	Gly	Asn	His	Ala
			20					25					30		
Ala	Gly	Ile	Leu	Thr	Leu	Gly	Lys	Arg	Arg	Pro	Gly	Pro	Pro	Gly	Leu
		35					40						45		

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Gln Gly Arg Leu Gln Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala
 50 55 60

Gly Ile Leu Thr Met Gly Arg Arg Ala Gly Ala Glu Leu Glu Pro Tyr
 65 70 75 80

Pro Cys Pro Gly Arg Arg Cys Pro Thr Ala Thr Ala Thr Ala Leu Ala
 85 90 95

Pro Arg Gly Gly Ser Arg Val
 100

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Leu Gly Val Asp Ala Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr
 1 5 10 15
 Cys Ser Cys Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala
 20 25 30
 Ala Gly Ile Leu Thr Leu Gly
 35

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Gly Val Asp Ala Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr
 1 5 10 15
 Cys Ser Cys Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala
 20 25 30
 Ala Gly Ile Leu Thr Leu
 35

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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln Arg Leu Leu Gln Ala
1 5 10 15

Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met Gly
20 25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln Arg Leu Leu Gln Ala
1 5 10 15

Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met
20 25

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala Ala Gly Ile
1 5 10 15
Leu Thr Leu Gly
20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Leu Gln Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala Gly Ile
1 5 10 15
Leu Thr Met Gly
20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Asn His Ala Ala Gly Ile Leu Thr
1 5